



#5/a

## SEQUENCE LISTING

<110> Bertin, John  
Robison, Keith E.

<120> NOVEL MOLECULES OF THE CARD-RELATED  
PROTEIN FAMILY AND USES THEREOF

<130> 07334-136001

<140> US 09/697,089

<141> 2000-10-26

<150> US 60/161,822

<151> 1999-10-27

<160> 12

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 3133

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (36)...(3107)

<400> 1

cgctctagcc cgggtgggaag ctttcatcca gaaca atg aat ttc ata aag gac 53  
Met Asn Phe Ile Lys Asp  
1 5

aat agc cga gcc ctt att caa aga atg gga atg act gtt ata aag caa 101  
Asn Ser Arg Ala Leu Ile Gln Arg Met Gly Met Thr Val Ile Lys Gln  
10 15 20

atc aca gat gac cta ttt gta tgg aat gtt ctg aat cgc gaa gaa gta 149  
Ile Thr Asp Asp Leu Phe Val Trp Asn Val Leu Asn Arg Glu Glu Val  
25 30 35

aac atc att tgc tgc gag aag gtg gag cag gat gct gct aga ggg atc 197  
Asn Ile Ile Cys Cys Glu Lys Val Glu Gln Asp Ala Ala Arg Gly Ile  
40 45 50

att cac atg att ttg aaa aag ggt tca gag tcc tgt aac ctc ttt ctt 245  
Ile His Met Ile Leu Lys Lys Gly Ser Glu Ser Cys Asn Leu Phe Leu  
55 60 65 70

aaa tcc ctt aag gag tgg aac tat cct cta ttt cag gac ttg aat gga 293  
Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu Phe Gln Asp Leu Asn Gly  
75 80 85

caa agt ctt ttt cat cag aca tca gaa gga gac ttg gac gat ttg gct 341

Gln Ser Leu Phe His Gln Thr Ser Glu Gly Asp Leu Asp Asp Leu Ala	
90 95 100	
cag gat tta aag gac ttg tac cat acc cca tct ttt ctg aac ttt tat	389
Gln Asp Leu Lys Asp Leu Tyr His Thr Pro Ser Phe Leu Asn Phe Tyr	
105 110 115	
ccc ctt ggt gaa gat att gac att att ttt aac ttg aaa agc acc ttc	437
Pro Leu Gly Glu Asp Ile Asp Ile Ile Phe Asn Leu Lys Ser Thr Phe	
120 125 130	
aca gaa cct gtc ctg tgg agg aag gac caa cac cat cac cgc gtg gag	485
Thr Glu Pro Val Leu Trp Arg Lys Asp Gln His His His Arg Val Glu	
135 140 145 150	
cag ctg acc ctg aat ggc ctc ctg cag gct ctt cag agc ccc tgc atc	533
Gln Leu Thr Leu Asn Gly Leu Leu Gln Ala Leu Gln Ser Pro Cys Ile	
155 160 165	
att gaa ggg gaa tct ggc aaa ggc aag tcc act ctg ctg cag cgc att	581
Ile Glu Gly Glu Ser Gly Lys Gly Lys Ser Thr Leu Leu Gln Arg Ile	
170 175 180	
gcc atg ctc tgg ggc tcc gga aag tgc aag gct ctg acc aag ttc aaa	629
Ala Met Leu Trp Gly Ser Gly Lys Cys Lys Ala Leu Thr Lys Phe Lys	
185 190 195	
ttc gtc ttc ttc ctc cgt ctc agc agg gcc cag ggt gga ctt ttt gaa	677
Phe Val Phe Phe Leu Arg Leu Ser Arg Ala Gln Gly Gly Leu Phe Glu	
200 205 210	
acc ctc tgt gat caa ctc ctg gat ata cct ggc aca atc agg aag cag	725
Thr Leu Cys Asp Gln Leu Leu Asp Ile Pro Gly Thr Ile Arg Lys Gln	
215 220 225 230	
aca ttc atg gcc atg ctg ctg aag ctg cgg cag agg gtt ctt ttc ctt	773
Thr Phe Met Ala Met Leu Leu Lys Leu Arg Gln Arg Val Leu Phe Leu	
235 240 245	
ctt gat ggc tac aat gaa ttc aag ccc cag aac tgc cca gaa atc gaa	821
Leu Asp Gly Tyr Asn Glu Phe Lys Pro Gln Asn Cys Pro Glu Ile Glu	
250 255 260	
gcc ctg ata aag gaa aac cac cgc ttc aag aac atg gtc atc gtc acc	869
Ala Leu Ile Lys Glu Asn His Arg Phe Lys Asn Met Val Ile Val Thr	
265 270 275	
act acc act gag tgc ctg agg cac ata cgg cag ttt ggt gcc ctg act	917
Thr Thr Thr Glu Cys Leu Arg His Ile Arg Gln Phe Gly Ala Leu Thr	
280 285 290	
gct gag gtg ggg gat atg aca gaa gac agc gcc cag gct ctc atc cga	965
Ala Glu Val Gly Asp Met Thr Glu Asp Ser Ala Gln Ala Leu Ile Arg	
295 300 305 310	
gaa gtg ctg atc aag gag ctt gct gaa ggc ttg ttg ctc caa att cag	1013
Glu Val Leu Ile Lys Glu Leu Ala Glu Gly Leu Leu Leu Gln Ile Gln	

315										320					325					
aaa tcc agg tgc ttg agg aat ctc atg aag acc cct ctc ttt gtg gtc	1061																			
Lys Ser Arg Cys Leu Arg Asn Leu Met Lys Thr Pro Leu Phe Val Val																				
330 335 340																				
atc act tgt gca atc cag atg ggt gaa agt gag ttc cac tct cac aca	1109																			
Ile Thr Cys Ala Ile Gln Met Gly Glu Ser Glu Phe His Ser His Thr																				
345 350 355																				
caa aca acg ctg ttc cat acc ttc tat gat ctg ttg ata cag aaa aac	1157																			
Gln Thr Thr Leu Phe His Thr Phe Tyr Asp Leu Leu Ile Gln Lys Asn																				
360 365 370																				
aaa cac aaa cat aaa ggt gtg gct gca agt gac ttc att cgg agc ctg	1205																			
Lys His Lys His Lys Gly Val Ala Ala Ser Asp Phe Ile Arg Ser Leu																				
375 380 385 390																				
gac cac tgt gga gac cta gct ctg gag ggt gtg ttc tcc cac aag ttt	1253																			
Asp His Cys Gly Asp Leu Ala Leu Glu Gly Val Phe Ser His Lys Phe																				
395 400 405																				
gat ttc gaa ctg cag gat gtg tcc agc gtg aat gag gat gtc ctg ctg	1301																			
Asp Phe Glu Leu Gln Asp Val Ser Ser Val Asn Glu Asp Val Leu Leu																				
410 415 420																				
aca act ggg ctc ctc tgt aaa tat aca gct caa agg ttc aag cca aag	1349																			
Thr Thr Gly Leu Leu Cys Lys Tyr Thr Ala Gln Arg Phe Lys Pro Lys																				
425 430 435																				
tat aaa ttc ttt cac aag tca ttc cag gag tac aca gca gga cga aga	1397																			
Tyr Lys Phe Phe His Lys Ser Phe Gln Glu Tyr Thr Ala Gly Arg Arg																				
440 445 450																				
ctc agc agt tta ttg acg tct cat gag cca gag gag gtg acc aag ggg	1445																			
Leu Ser Ser Leu Leu Thr Ser His Glu Pro Glu Glu Val Thr Lys Gly																				
455 460 465 470																				
aat ggt tac ttg cag aaa atg gtt tcc att tcg gac att aca tcc act	1493																			
Asn Gly Tyr Leu Gln Lys Met Val Ser Ile Ser Asp Ile Thr Ser Thr																				
475 480 485																				
tat agc agc ctg ctc cgg tac acc tgt ggg tca tct gtg gaa gcc acc	1541																			
Tyr Ser Ser Leu Leu Arg Tyr Thr Cys Gly Ser Ser Val Glu Ala Thr																				
490 495 500																				
agg gct gtt atg aag cac ctc gca gca gtg tat caa cac ggc tgc ctt	1589																			
Arg Ala Val Met Lys His Leu Ala Ala Val Tyr Gln His Gly Cys Leu																				
505 510 515																				
ctc gga ctt tcc atc gcc aag agg cct ctc tgg aga cag gaa tct ttg	1637																			
Leu Gly Leu Ser Ile Ala Lys Arg Pro Leu Trp Arg Gln Glu Ser Leu																				
520 525 530																				
caa agt gtg aaa aac acc act gag caa gaa att ctg aaa gcc ata aac	1685																			
Gln Ser Val Lys Asn Thr Thr Glu Gln Glu Ile Leu Lys Ala Ile Asn																				
535 540 545 550																				

atc aat tcc ttt gta gag tgt ggc atc cat tta tat caa gag agt aca Ile Asn Ser Phe Val Glu Cys Gly Ile His Leu Tyr Gln Glu Ser Thr 555 560 565	1733
tcc aaa tca gcc ctg agc caa gaa ttt gaa gct ttc ttt caa ggt aaa Ser Lys Ser Ala Leu Ser Gln Glu Phe Glu Ala Phe Phe Gln Gly Lys 570 575 580	1781
agc tta tat atc aac tca ggg aac atc ccc gat tac tta ttt gac ttc Ser Leu Tyr Ile Asn Ser Gly Asn Ile Pro Asp Tyr Leu Phe Asp Phe 585 590 595	1829
ttt gaa cat ttg ccc aat tgt gca agt gct ctg gac ttc att aaa ctg Phe Glu His Leu Pro Asn Cys Ala Ser Ala Leu Asp Phe Ile Lys Leu 600 605 610	1877
gac ttt tat ggg gga gct atg gct tca tgg gaa aag gct gca gaa gac Asp Phe Tyr Gly Gly Ala Met Ala Ser Trp Glu Lys Ala Ala Glu Asp 615 620 625 630	1925
aca ggt gga atc cac atg gaa gag gcc cca gaa acc tac att ccc agc Thr Gly Gly Ile His Met Glu Glu Ala Pro Glu Thr Tyr Ile Pro Ser 635 640 645	1973
agg gct gta tct ttg ttc ttc aac tgg aag cag gaa ttc agg act ctg Arg Ala Val Ser Leu Phe Phe Asn Trp Lys Gln Glu Phe Arg Thr Leu 650 655 660	2021
gag gtc aca ctc cgg gat ttc agc aag ttg aat aag caa gat atc aca Glu Val Thr Leu Arg Asp Phe Ser Lys Leu Asn Lys Gln Asp Ile Thr 665 670 675	2069
tat ctg ggg aaa ata ttc agc tct gcc aca agc ctc agg ctg caa ata Tyr Leu Gly Lys Ile Phe Ser Ser Ala Thr Ser Leu Arg Leu Gln Ile 680 685 690	2117
aag aga tgt gct ggt gtg gct gga agc ctc agt ttg gtc ctc agc acc Lys Arg Cys Ala Gly Val Ala Gly Ser Leu Ser Leu Val Leu Ser Thr 695 700 705 710	2165
tgt aag aac att tat tct ctc atg gtg gaa gcc agt ccc ctc acc ata Cys Lys Asn Ile Tyr Ser Leu Met Val Glu Ala Ser Pro Leu Thr Ile 715 720 725	2213
gaa gat gag agg cac atc aca tct gta aca aac ctg aaa acc ttg agt Glu Asp Glu Arg His Ile Thr Ser Val Thr Asn Leu Lys Thr Leu Ser 730 735 740	2261
att cat gac cta cag aat caa cgg ctg ccg ggt ggt ctg act gac agc Ile His Asp Leu Gln Asn Gln Arg Leu Pro Gly Gly Leu Thr Asp Ser 745 750 755	2309
ttg ggt aac ttg aag aac ctt aca aag ctc ata atg gat aac ata aag Leu Gly Asn Leu Lys Asn Leu Thr Lys Leu Ile Met Asp Asn Ile Lys 760 765 770	2357

atg aat gaa gaa gat gct ata aaa cta gct gaa ggc ctg aaa aac ctg Met Asn Glu Glu Asp Ala Ile Lys Leu Ala Glu Gly Leu Lys Asn Leu 775 780 785 790	2405
aag aag atg tgt tta ttt cat ttg acc cac ttg tct gac att gga gag Lys Lys Met Cys Leu Phe His Leu Thr His Leu Ser Asp Ile Gly Glu 795 800 805	2453
gga atg gat tac ata gtc aag tct ctg tca agt gaa ccc tgt gac ctt Gly Met Asp Tyr Ile Val Lys Ser Leu Ser Ser Glu Pro Cys Asp Leu 810 815 820	2501
gaa gaa att caa tta gtc tcc tgc tgc ttg tct gca aat gca gtg aaa Glu Glu Ile Gln Leu Val Ser Cys Cys Leu Ser Ala Asn Ala Val Lys 825 830 835	2549
atc cta gct cag aat ctt cac aat ttg gtc aaa ctg agc att ctt gat Ile Leu Ala Gln Asn Leu His Asn Leu Val Lys Leu Ser Ile Leu Asp 840 845 850	2597
tta tca gaa aat tac ctg gaa aaa gat gga aat gaa gct ctt cat gaa Leu Ser Glu Asn Tyr Leu Glu Lys Asp Gly Asn Glu Ala Leu His Glu 855 860 865 870	2645
ctg atc gac agg atg aac gtg cta gaa cag ctc acc gca ctg atg ctg Leu Ile Asp Arg Met Asn Val Leu Glu Gln Leu Thr Ala Leu Met Leu 875 880 885	2693
ccc tgg ggc tgt gac gtg caa ggc agc ctg agc agc ctg ttg aaa cat Pro Trp Gly Cys Asp Val Gln Gly Ser Leu Ser Ser Leu Leu Lys His 890 895 900	2741
ttg gag gag gtc cca caa ctc gtc aag ctt ggg ttg aaa aac tgg aga Leu Glu Glu Val Pro Gln Leu Val Lys Leu Gly Leu Lys Asn Trp Arg 905 910 915	2789
ctc aca gat aca gag att aga att tta ggt gca ttt ttt gga aag aac Leu Thr Asp Thr Glu Ile Arg Ile Leu Gly Ala Phe Phe Gly Lys Asn 920 925 930	2837
cct ctg aaa aac ttc cag cag ttg aat ttg gcg gga aat cgt gtg agc Pro Leu Lys Asn Phe Gln Gln Leu Asn Leu Ala Gly Asn Arg Val Ser 935 940 945 950	2885
agt gat gga tgg ctt gcc ttc atg ggt gta ttt gag aat ctt aag caa Ser Asp Gly Trp Leu Ala Phe Met Gly Val Phe Glu Asn Leu Lys Gln 955 960 965	2933
tta gtg ttt ttt gac ttt agt act aaa gaa ttt cta cct gat cca gca Leu Val Phe Phe Asp Phe Ser Thr Lys Glu Phe Leu Pro Asp Pro Ala 970 975 980	2981
tta gtc aga aaa ctt agc caa gtg tta tcc aag tta act ttt ctg caa Leu Val Arg Lys Leu Ser Gln Val Leu Ser Lys Leu Thr Phe Leu Gln 985 990 995	3029
gaa gct agg ctt gtt ggg tgg caa ttt gat gat gat gat ctc agt gtt	3077

Glu Ala Arg Leu Val Gly Trp Gln Phe Asp Asp Asp Asp Leu Ser Val  
 1000 1005 1010

att aca ggt gct ttt aaa cta gta act gct taaataaaagt gtactcgaag 3127  
 Ile Thr Gly Ala Phe Lys Leu Val Thr Ala  
 1015 1020

ccagta 3133

<210> 2  
 <211> 1024  
 <212> PRT  
 <213> Homo sapiens

<400> 2  
 Met Asn Phe Ile Lys Asp Asn Ser Arg Ala Leu Ile Gln Arg Met Gly  
 1 5 10 15  
 Met Thr Val Ile Lys Gln Ile Thr Asp Asp Leu Phe Val Trp Asn Val  
 20 25 30  
 Leu Asn Arg Glu Glu Val Asn Ile Ile Cys Cys Glu Lys Val Glu Gln  
 35 40 45  
 Asp Ala Ala Arg Gly Ile Ile His Met Ile Leu Lys Lys Gly Ser Glu  
 50 55 60  
 Ser Cys Asn Leu Phe Leu Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu  
 65 70 75 80  
 Phe Gln Asp Leu Asn Gly Gln Ser Leu Phe His Gln Thr Ser Glu Gly  
 85 90 95  
 Asp Leu Asp Asp Leu Ala Gln Asp Leu Lys Asp Leu Tyr His Thr Pro  
 100 105 110  
 Ser Phe Leu Asn Phe Tyr Pro Leu Gly Glu Asp Ile Asp Ile Ile Phe  
 115 120 125  
 Asn Leu Lys Ser Thr Phe Thr Glu Pro Val Leu Trp Arg Lys Asp Gln  
 130 135 140  
 His His His Arg Val Glu Gln Leu Thr Leu Asn Gly Leu Leu Gln Ala  
 145 150 155 160  
 Leu Gln Ser Pro Cys Ile Ile Glu Gly Glu Ser Gly Lys Gly Lys Ser  
 165 170 175  
 Thr Leu Leu Gln Arg Ile Ala Met Leu Trp Gly Ser Gly Lys Cys Lys  
 180 185 190  
 Ala Leu Thr Lys Phe Lys Phe Val Phe Phe Leu Arg Leu Ser Arg Ala  
 195 200 205  
 Gln Gly Gly Leu Phe Glu Thr Leu Cys Asp Gln Leu Leu Asp Ile Pro  
 210 215 220  
 Gly Thr Ile Arg Lys Gln Thr Phe Met Ala Met Leu Leu Lys Leu Arg  
 225 230 235 240  
 Gln Arg Val Leu Phe Leu Leu Asp Gly Tyr Asn Glu Phe Lys Pro Gln  
 245 250 255  
 Asn Cys Pro Glu Ile Glu Ala Leu Ile Lys Glu Asn His Arg Phe Lys  
 260 265 270  
 Asn Met Val Ile Val Thr Thr Thr Thr Glu Cys Leu Arg His Ile Arg  
 275 280 285  
 Gln Phe Gly Ala Leu Thr Ala Glu Val Gly Asp Met Thr Glu Asp Ser  
 290 295 300  
 Ala Gln Ala Leu Ile Arg Glu Val Leu Ile Lys Glu Leu Ala Glu Gly  
 305 310 315 320  
 Leu Leu Leu Gln Ile Gln Lys Ser Arg Cys Leu Arg Asn Leu Met Lys  
 325 330 335

Thr	Pro	Leu	Phe	Val	Val	Ile	Thr	Cys	Ala	Ile	Gln	Met	Gly	Glu	Ser
			340					345					350		
Glu	Phe	His	Ser	His	Thr	Gln	Thr	Thr	Leu	Phe	His	Thr	Phe	Tyr	Asp
		355					360				365				
Leu	Leu	Ile	Gln	Lys	Asn	Lys	His	Lys	His	Lys	Gly	Val	Ala	Ala	Ser
	370				375						380				
Asp	Phe	Ile	Arg	Ser	Leu	Asp	His	Cys	Gly	Asp	Leu	Ala	Leu	Glu	Gly
385					390					395					400
Val	Phe	Ser	His	Lys	Phe	Asp	Phe	Glu	Leu	Gln	Asp	Val	Ser	Ser	Val
			405					410						415	
Asn	Glu	Asp	Val	Leu	Leu	Thr	Thr	Gly	Leu	Leu	Cys	Lys	Tyr	Thr	Ala
		420						425					430		
Gln	Arg	Phe	Lys	Pro	Lys	Tyr	Lys	Phe	Phe	His	Lys	Ser	Phe	Gln	Glu
	435						440				445				
Tyr	Thr	Ala	Gly	Arg	Arg	Leu	Ser	Ser	Leu	Leu	Thr	Ser	His	Glu	Pro
	450					455				460					
Glu	Glu	Val	Thr	Lys	Gly	Asn	Gly	Tyr	Leu	Gln	Lys	Met	Val	Ser	Ile
465					470					475					480
Ser	Asp	Ile	Thr	Ser	Thr	Tyr	Ser	Ser	Leu	Leu	Arg	Tyr	Thr	Cys	Gly
			485					490					495		
Ser	Ser	Val	Glu	Ala	Thr	Arg	Ala	Val	Met	Lys	His	Leu	Ala	Ala	Val
		500						505					510		
Tyr	Gln	His	Gly	Cys	Leu	Leu	Gly	Leu	Ser	Ile	Ala	Lys	Arg	Pro	Leu
	515						520					525			
Trp	Arg	Gln	Glu	Ser	Leu	Gln	Ser	Val	Lys	Asn	Thr	Thr	Glu	Gln	Glu
	530					535					540				
Ile	Leu	Lys	Ala	Ile	Asn	Ile	Asn	Ser	Phe	Val	Glu	Cys	Gly	Ile	His
545					550					555					560
Leu	Tyr	Gln	Glu	Ser	Thr	Ser	Lys	Ser	Ala	Leu	Ser	Gln	Glu	Phe	Glu
			565					570						575	
Ala	Phe	Phe	Gln	Gly	Lys	Ser	Leu	Tyr	Ile	Asn	Ser	Gly	Asn	Ile	Pro
	580							585					590		
Asp	Tyr	Leu	Phe	Asp	Phe	Phe	Glu	His	Leu	Pro	Asn	Cys	Ala	Ser	Ala
	595						600					605			
Leu	Asp	Phe	Ile	Lys	Leu	Asp	Phe	Tyr	Gly	Gly	Ala	Met	Ala	Ser	Trp
	610					615					620				
Glu	Lys	Ala	Ala	Glu	Asp	Thr	Gly	Gly	Ile	His	Met	Glu	Glu	Ala	Pro
625					630					635					640
Glu	Thr	Tyr	Ile	Pro	Ser	Arg	Ala	Val	Ser	Leu	Phe	Phe	Asn	Trp	Lys
			645					650					655		
Gln	Glu	Phe	Arg	Thr	Leu	Glu	Val	Thr	Leu	Arg	Asp	Phe	Ser	Lys	Leu
		660						665					670		
Asn	Lys	Gln	Asp	Ile	Thr	Tyr	Leu	Gly	Lys	Ile	Phe	Ser	Ser	Ala	Thr
	675						680					685			
Ser	Leu	Arg	Leu	Gln	Ile	Lys	Arg	Cys	Ala	Gly	Val	Ala	Gly	Ser	Leu
	690					695					700				
Ser	Leu	Val	Leu	Ser	Thr	Cys	Lys	Asn	Ile	Tyr	Ser	Leu	Met	Val	Glu
705					710					715					720
Ala	Ser	Pro	Leu	Thr	Ile	Glu	Asp	Glu	Arg	His	Ile	Thr	Ser	Val	Thr
			725					730						735	
Asn	Leu	Lys	Thr	Leu	Ser	Ile	His	Asp	Leu	Gln	Asn	Gln	Arg	Leu	Pro
		740						745					750		
Gly	Gly	Leu	Thr	Asp	Ser	Leu	Gly	Asn	Leu	Lys	Asn	Leu	Thr	Lys	Leu
		755					760					765			
Ile	Met	Asp	Asn	Ile	Lys	Met	Asn	Glu	Glu	Asp	Ala	Ile	Lys	Leu	Ala
	770					775				780					
Glu	Gly	Leu	Lys	Asn	Leu	Lys	Lys	Met	Cys	Leu	Phe	His	Leu	Thr	His

785		790		795		800
Leu Ser Asp Ile Gly	Glu Gly Met Asp Tyr Ile Val Lys Ser Leu Ser					
	805		810			815
Ser Glu Pro Cys Asp	Leu Glu Glu Ile Gln Leu Val Ser Cys Cys Leu					
	820		825			830
Ser Ala Asn Ala Val	Lys Ile Leu Ala Gln Asn Leu His Asn Leu Val					
	835		840			845
Lys Leu Ser Ile Leu	Asp Leu Ser Glu Asn Tyr Leu Glu Lys Asp Gly					
	850		855			860
Asn Glu Ala Leu His	Glu Leu Ile Asp Arg Met Asn Val Leu Glu Gln					
	865		870			875
Leu Thr Ala Leu Met	Leu Pro Trp Gly Cys Asp Val Gln Gly Ser Leu					
	885		890			895
Ser Ser Leu Leu Lys	His Leu Glu Glu Val Pro Gln Leu Val Lys Leu					
	900		905			910
Gly Leu Lys Asn Trp	Arg Leu Thr Asp Thr Glu Ile Arg Ile Leu Gly					
	915		920			925
Ala Phe Phe Gly Lys	Asn Pro Leu Lys Asn Phe Gln Gln Leu Asn Leu					
	930		935			940
Ala Gly Asn Arg Val	Ser Ser Asp Gly Trp Leu Ala Phe Met Gly Val					
	945		950			955
Phe Glu Asn Leu Lys	Gln Leu Val Phe Phe Asp Phe Ser Thr Lys Glu					
	965		970			975
Phe Leu Pro Asp Pro	Ala Leu Val Arg Lys Leu Ser Gln Val Leu Ser					
	980		985			990
Lys Leu Thr Phe Leu	Gln Glu Ala Arg Leu Val Gly Trp Gln Phe Asp					
	995		1000			1005
Asp Asp Asp Leu Ser	Val Ile Thr Gly Ala Phe Lys Leu Val Thr Ala					
	1010		1015			1020

&lt;210&gt; 3

&lt;211&gt; 3072

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3

atgaatttca	taaaggacaa	tagccgagcc	cttattcaaa	gaatgggaat	gactgttata	60
aagcaaatca	cagatgacct	atttgatatg	aatgttctga	atcgcggaaga	agtaaacaatc	120
atttgctgcg	agaagggtgga	gcaggatgct	gctagaggga	tcattcacat	gattttgaaa	180
aagggttcag	agtccgtgaa	cctctttctt	aaatccctta	aggagtggaa	ctatccctcta	240
tttcaggact	tgaatggaca	aagtcttttt	catcagacat	cagaaggaga	cttgacgat	300
ttggctcagg	atttaaagga	cttgtaccat	accccatctt	ttctgaactt	ttatccccctt	360
ggtgaagata	ttgacattat	ttttaacttg	aaaagcacct	tcacagaacc	tgctcgtgtg	420
aggaaggacc	aacaccatca	ccgcgtggag	cagctgaccc	tgaatggcct	cctgcaggct	480
cttcagagcc	cctgcatcat	tgaaggggaa	tctggcaaag	gcaagtccac	tctgctgcag	540
cgcattgcca	tgctctgggg	ctccggaaa	tgcaaggctc	tgaccaagtt	caaattcgtc	600
ttcttctctc	gtctcagcag	ggcccagggt	ggactttttg	aaaccctctg	tgatcaactc	660
ctggatatac	ctggcacaa	caggaagcag	acattcatgg	ccatgctgct	gaagctgcgg	720
cagagggttc	ttttctctct	tgatggctac	aatgaattca	agccccagaa	ctgcccagaa	780
atcgaagccc	tgataaagga	aaaccaccgc	ttcaagaaca	tggtcatcgt	caccactacc	840
actgagtgcc	tgaggcacat	acggcagttt	ggtgccctga	ctgctgagg	gggggatatg	900
acagaagaca	gcgcccaggc	tctcatccga	gaagtgtgta	tcaaggagct	tgctgaaggc	960
ttgttgctcc	aaattcagaa	atccagggtg	ttgaggaatc	tcatgaagac	ccctctcttt	1020
gtgggtcatca	cttgtgcaat	ccagatgggt	gaaagtgagt	tccactctca	cacacaaaca	1080
acgctgttcc	ataccttcta	tgatctgttg	atacagaaaa	acaaacacaa	acataaagg	1140
gtggctgcaa	gtgacttcat	tccgagcctg	gaccactgtg	gagacctagc	tctggagggt	1200
gtgttctccc	acaagtttga	tttcgaactg	caggatgtgt	ccagcgtgaa	tgaggatgtc	1260



```

ctgctgacaa ctgggctcct ctgtaaatat acagctcaaa ggttcaagcc aaagtataaa 1320
ttctttcaca agtcattcca ggagtacaca gcaggacgaa gactcagcag tttattgacg 1380
tctcatgagc cagaggaggt gaccaagggg aatgggtact tgcagaaaat ggtttccatt 1440
tcggacatta catccactta tagcagcctg ctccggtaca cctgtgggtc atctgtggaa 1500
gccaccaggg ctgttatgaa gcacctcgca gcagtgtatc aacacggctg ccttctcgga 1560
ctttccatcg ccaagaggcc tctctggaga caggaatctt tgcaaagtgt gaaaaacacc 1620
actgagcaag aaattctgaa agccataaac atcaattcct ttgtagagtg tggcatccat 1680
ttatatcaag agagtacatc caaatcagcc ctgagccaag aatttgaagc tttctttcaa 1740
ggtaaaagct tatatatcaa ctcaggggaa atccccgatt acttatttga cttctttgaa 1800
catttgccca attgtgcaag tgctctggac ttcattaaac tggactttta tgggggagct 1860
atggcttcat gggaaaaggc tgcagaagac acagggtggaa tccacatgga agaggcccca 1920
gaaacctaca ttcccagcag ggctgtatct ttgttcttca actggaagca ggaattcagg 1980
actctggagg tcacactccg ggatttcagc aagttgaata agcaagatat cacatatctg 2040
gggaaaatat tcagctctgc cacaagcctc aggctgcaaa taaagagatg tgctggtgtg 2100
gctggaagcc tcagtttggg cctcagcacc tgtaagaaca tttattctct catggtggaa 2160
gccagtcccc tcaccataga agatgagagg cacatcacat ctgtaacaaa cctgaaaacc 2220
ttgagtattc atgacctaca gaatcaacgg ctgccgggtg gtctgactga cagcttgggt 2280
aacttgaaga accttacaaa gctcataatg gataacataa agatgaatga agaagatgct 2340
ataaaactag ctgaaggcct gaaaaacctg aagaagatgt gtttatttca tttgaccac 2400
ttgtctgaca ttggagaggg aatggattac atagtcaagt ctctgtcaag tgaaccctgt 2460
gaccttgaag aaattcaatt agtctcctgc tgcttgtctg caaatgcagt gaaaatccta 2520
gctcagaatc ttcacaattt ggtcaaaactg agcattcttg atttatcaga aaattacctg 2580
gaaaaagatg gaaatgaagc tcttcatgaa ctgatcgaca ggatgaacgt gctagaacag 2640
ctcaccgcac tgatgctgcc ctggggctgt gacgtgcaag gcagcctgag cagcctgttg 2700
aaacatttgg aggaggtccc acaactcgtc aagcttgggt tgaaaaactg gagactcaca 2760
gatacagaga ttagaatttt aggtgcattt tttggaaaga accctctgaa aaacttccag 2820
cagttgaatt tggcgggaaa tcgtgtgagc agtgatggat ggcttgccct catgggtgta 2880
tttgagaatc ttaagcaatt agtgtttttt gactttagta ctaaagaatt tctacctgat 2940
ccagcattag tcagaaaact tagccaagtg ttatccaagt taacttttct gcaagaagct 3000
aggcttggtg ggtggcaatt tgatgatgat gatctcagtg ttattacagg tgctttttaa 3060
ctagtaactg ct 3072

```

```

<210> 4
<211> 3615
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (1)...(3612)

```

```

<400> 4
atg ctg aac gct ggt ccc ctg ggc tcc ctt att tct ttc tct ata ctt 48
Met Leu Asn Ala Gly Pro Leu Gly Ser Leu Ile Ser Phe Ser Ile Leu
1 5 10 15

tgt ctc tgt gtc ttt ttc ttt tcc aag tct ctc gtt cca cct aac gag 96
Cys Leu Cys Val Phe Phe Phe Ser Lys Ser Leu Val Pro Pro Asn Glu
20 25 30

aaa cac cca cag aac aag aag gta tct ggt cta caa gaa ctc gag gcc 144
Lys His Pro Gln Asn Lys Lys Val Ser Gly Leu Gln Glu Leu Glu Ala
35 40 45

tca ctg aaa cgg aaa gca aat aca aag aaa ctt tat ttt aaa aac atg 192
Ser Leu Lys Arg Lys Ala Asn Thr Lys Lys Leu Tyr Phe Lys Asn Met
50 55 60

```

tct tgg tct ccc aag aag agg gca att gga ttg ctc agc cag aga ccc	240
Ser Trp Ser Pro Lys Lys Arg Ala Ile Gly Leu Leu Ser Gln Arg Pro	
65 70 75 80	
ttg cag gca gac aca caa gcg gct gga cgt cga gag gaa cac atc ggc	288
Leu Gln Ala Asp Thr Gln Ala Ala Gly Arg Arg Glu Glu His Ile Gly	
85 90 95	
gga aga aca tac aag cag ctg gac gtc cag agg acg ttg aag gga gaa	336
Gly Arg Thr Tyr Lys Gln Leu Asp Val Gln Arg Thr Leu Lys Gly Glu	
100 105 110	
tgc tgg cgg aag agc aca caa cag aca tcg gca cgc cag cag gcc atc	384
Cys Trp Arg Lys Ser Thr Gln Gln Thr Ser Ala Arg Gln Gln Ala Ile	
115 120 125	
cac cag agg aac gac tcg gag ttt ggc ctg gag gtg aat ttc ata aag	432
His Gln Arg Asn Asp Ser Glu Phe Gly Leu Glu Val Asn Phe Ile Lys	
130 135 140	
gac aat agc cga gcc ctt att caa aga atg gga atg act gtt ata aag	480
Asp Asn Ser Arg Ala Leu Ile Gln Arg Met Gly Met Thr Val Ile Lys	
145 150 155 160	
caa atc aca gat gac cta ttt gta tgg aat gtt ctg aat cgc gaa gaa	528
Gln Ile Thr Asp Asp Leu Phe Val Trp Asn Val Leu Asn Arg Glu Glu	
165 170 175	
gta aac atc att tgc tgc gag aag gtg gag cag gat gct gct aga ggg	576
Val Asn Ile Ile Cys Cys Glu Lys Val Glu Gln Asp Ala Ala Arg Gly	
180 185 190	
atc att cac atg att ttg aaa aag ggt tca gag tcc tgt aac ctc ttt	624
Ile Ile His Met Ile Leu Lys Lys Gly Ser Glu Ser Cys Asn Leu Phe	
195 200 205	
ctt aaa tcc ctt aag gag tgg aac tat cct cta ttt cag gac ttg aat	672
Leu Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu Phe Gln Asp Leu Asn	
210 215 220	
gga caa agt ttt gag gag aca cag aat tgg gtc ttc ttt aac atc acc	720
Gly Gln Ser Phe Glu Glu Thr Gln Asn Trp Val Phe Phe Asn Ile Thr	
225 230 235 240	
tct tct cta ata ggt ctt ttt cat cag aca tca gaa gga gac ttg gac	768
Ser Ser Leu Ile Gly Leu Phe His Gln Thr Ser Glu Gly Asp Leu Asp	
245 250 255	
gat ttg gct cag gat tta aag gac ttg tac cat acc cca tct ttt ctg	816
Asp Leu Ala Gln Asp Leu Lys Asp Leu Tyr His Thr Pro Ser Phe Leu	
260 265 270	
aac ttt tat ccc ctt ggt gaa gat att gac att att ttt aac ttg aaa	864
Asn Phe Tyr Pro Leu Gly Glu Asp Ile Asp Ile Ile Phe Asn Leu Lys	
275 280 285	

agc acc ttc aca gaa cct gtc ctg tgg agg aag gac caa cac cat cac	912
Ser Thr Phe Thr Glu Pro Val Leu Trp Arg Lys Asp Gln His His His	
290 295 300	
cgc gtg gag cag ctg acc ctg aat ggc ctc ctg cag gct ctt cag agc	960
Arg Val Glu Gln Leu Thr Leu Asn Gly Leu Leu Gln Ala Leu Gln Ser	
305 310 315 320	
ccc tgc atc att gaa ggg gaa tct ggc aaa ggc aag tcc act ctg ctg	1008
Pro Cys Ile Ile Glu Gly Glu Ser Gly Lys Gly Lys Ser Thr Leu Leu	
325 330 335	
cag cga att gcc atg ctc tgg ggc tcc gga aag tgc aag gct ctg acc	1056
Gln Arg Ile Ala Met Leu Trp Gly Ser Gly Lys Cys Lys Ala Leu Thr	
340 345 350	
aag ttc aaa ttc gtc ttc ttc ctc cgt ctc agc agg gcc cag ggt gga	1104
Lys Phe Lys Phe Val Phe Phe Leu Arg Leu Ser Arg Ala Gln Gly Gly	
355 360 365	
ctt ttt gaa acc ctc tgt gat caa ctc ctg gat ata cct ggc aca atc	1152
Leu Phe Glu Thr Leu Cys Asp Gln Leu Leu Asp Ile Pro Gly Thr Ile	
370 375 380	
agg aag cag aca ttc atg gcc atg ctg ctg aag ctg cgg cag agg gtt	1200
Arg Lys Gln Thr Phe Met Ala Met Leu Leu Lys Leu Arg Gln Arg Val	
385 390 395 400	
ctt ttc ctt ctt gat ggc tac aat gaa ttc aag ccc cag aac tgc cca	1248
Leu Phe Leu Leu Asp Gly Tyr Asn Glu Phe Lys Pro Gln Asn Cys Pro	
405 410 415	
gaa atc gaa gcc ctg ata aag gaa aac cac cgc ttc aag aac atg gtc	1296
Glu Ile Glu Ala Leu Ile Lys Glu Asn His Arg Phe Lys Asn Met Val	
420 425 430	
atc gtc acc act acc act gag tgc ctg agg cac ata cgg cag ttt ggt	1344
Ile Val Thr Thr Thr Thr Glu Cys Leu Arg His Ile Arg Gln Phe Gly	
435 440 445	
gcc ctg act gct gag gtg ggg gat atg aca gaa gac agc gcc cag gct	1392
Ala Leu Thr Ala Glu Val Gly Asp Met Thr Glu Asp Ser Ala Gln Ala	
450 455 460	
ctc atc cga gaa gtg ctg atc aag gag ctt gct gaa ggc ttg ttg ctc	1440
Leu Ile Arg Glu Val Leu Ile Lys Glu Leu Ala Glu Gly Leu Leu Leu	
465 470 475 480	
caa att cag aaa tcc agg tgc ttg agg aat ctc atg aag acc cct ctc	1488
Gln Ile Gln Lys Ser Arg Cys Leu Arg Asn Leu Met Lys Thr Pro Leu	
485 490 495	
ttt gtg gtc atc act tgt gca atc cag atg ggt gaa agt gag ttc cac	1536
Phe Val Val Ile Thr Cys Ala Ile Gln Met Gly Glu Ser Glu Phe His	
500 505 510	
tct cac aca caa aca acg ctg ttc cat acc ttc tat gat ctg ttg ata	1584

Ser	His	Thr	Gln	Thr	Thr	Leu	Phe	His	Thr	Phe	Tyr	Asp	Leu	Leu	Ile	
		515					520					525				
cag	aaa	aac	aaa	cac	aaa	cat	aaa	ggg	gtg	gct	gca	agt	gac	ttc	att	1632
Gln	Lys	Asn	Lys	His	Lys	His	Lys	Gly	Val	Ala	Ala	Ser	Asp	Phe	Ile	
	530					535				540						
cgg	agc	ctg	gac	cac	tgt	gga	gac	cta	gct	ctg	gag	ggg	gtg	ttc	tcc	1680
Arg	Ser	Leu	Asp	His	Cys	Gly	Asp	Leu	Ala	Leu	Glu	Gly	Val	Phe	Ser	
545					550				555						560	
cac	aag	ttt	gat	ttc	gaa	ctg	cag	gat	gtg	tcc	agc	gtg	aat	gag	gat	1728
His	Lys	Phe	Asp	Phe	Glu	Leu	Gln	Asp	Val	Ser	Ser	Val	Asn	Glu	Asp	
				565					570					575		
gtc	ctg	ctg	aca	act	ggg	ctc	ctc	tgt	aaa	tat	aca	gct	caa	agg	ttc	1776
Val	Leu	Leu	Thr	Thr	Gly	Leu	Leu	Cys	Lys	Tyr	Thr	Ala	Gln	Arg	Phe	
			580					585					590			
aag	cca	aag	tat	aaa	ttc	ttt	cac	aag	tca	ttc	cag	gag	tac	aca	gca	1824
Lys	Pro	Lys	Tyr	Lys	Phe	Phe	His	Lys	Ser	Phe	Gln	Glu	Tyr	Thr	Ala	
	595						600					605				
gga	cga	aga	ctc	agc	agt	tta	ttg	acg	tct	cat	gag	cca	gag	gag	gtg	1872
Gly	Arg	Arg	Leu	Ser	Ser	Leu	Leu	Thr	Ser	His	Glu	Pro	Glu	Glu	Val	
	610					615					620					
acc	aag	ggg	aat	ggg	tac	ttg	cag	aaa	atg	gtt	tcc	att	tcg	gac	att	1920
Thr	Lys	Gly	Asn	Gly	Tyr	Leu	Gln	Lys	Met	Val	Ser	Ile	Ser	Asp	Ile	
625					630					635					640	
aca	tcc	act	tat	agc	agc	ctg	ctc	cgg	tac	acc	tgt	ggg	tca	tct	gtg	1968
Thr	Ser	Thr	Tyr	Ser	Ser	Leu	Leu	Arg	Tyr	Thr	Cys	Gly	Ser	Ser	Val	
				645					650					655		
gaa	gcc	acc	agg	gct	gtt	atg	aag	cac	ctc	gca	gca	gtg	tat	caa	cac	2016
Glu	Ala	Thr	Arg	Ala	Val	Met	Lys	His	Leu	Ala	Ala	Val	Tyr	Gln	His	
			660					665					670			
ggc	tgc	ctt	ctc	gga	ctt	tcc	atc	gcc	aag	agg	cct	ctc	tggt	aga	cag	2064
Gly	Cys	Leu	Leu	Gly	Leu	Ser	Ile	Ala	Lys	Arg	Pro	Leu	Trp	Arg	Gln	
		675					680					685				
gaa	tct	ttg	caa	agt	gtg	aaa	aac	acc	act	gag	caa	gaa	att	ctg	aaa	2112
Glu	Ser	Leu	Gln	Ser	Val	Lys	Asn	Thr	Thr	Glu	Gln	Glu	Ile	Leu	Lys	
	690					695					700					
gcc	ata	aac	atc	aat	tcc	ttt	gta	gag	tgt	ggc	atc	cat	tta	tat	caa	2160
Ala	Ile	Asn	Ile	Asn	Ser	Phe	Val	Glu	Cys	Gly	Ile	His	Leu	Tyr	Gln	
705					710					715					720	
gag	agt	aca	tcc	aaa	tca	gcc	ctg	agc	caa	gaa	ttt	gaa	gct	ttc	ttt	2208
Glu	Ser	Thr	Ser	Lys	Ser	Ala	Leu	Ser	Gln	Glu	Phe	Glu	Ala	Phe	Phe	
				725					730					735		
caa	ggg	aaa	agc	tta	tat	atc	aac	tca	ggg	aac	atc	ccc	gat	tac	tta	2256
Gln	Gly	Lys	Ser	Leu	Tyr	Ile	Asn	Ser	Gly	Asn	Ile	Pro	Asp	Tyr	Leu	

740						745						750						
ttt gac ttc ttt gaa cat ttg ccc aat tgt gca agt gcc ctg gac ttc	2304																	
Phe Asp Phe Phe Glu His Leu Pro Asn Cys Ala Ser Ala Leu Asp Phe																		
755 760 765																		
att aaa ctg gac ttt tat ggg gga gct atg gct tca tgg gaa aag gct	2352																	
Ile Lys Leu Asp Phe Tyr Gly Gly Ala Met Ala Ser Trp Glu Lys Ala																		
770 775 780																		
gca gaa gac aca ggt gga atc cac atg gaa gag gcc cca gaa acc tac	2400																	
Ala Glu Asp Thr Gly Gly Ile His Met Glu Glu Ala Pro Glu Thr Tyr																		
785 790 795																		
att ccc agc agg gct gta tct ttg ttc ttc aac tgg aag cag gaa ttc	2448																	
Ile Pro Ser Arg Ala Val Ser Leu Phe Phe Asn Trp Lys Gln Glu Phe																		
805 810 815																		
agg act ctg gag gtc aca ctc cgg gat ttc agc aag ttg aat aag caa	2496																	
Arg Thr Leu Glu Val Thr Leu Arg Asp Phe Ser Lys Leu Asn Lys Gln																		
820 825 830																		
gat atc aga tat ctg ggg aaa ata ttc agc tct gcc aca agc ctc agg	2544																	
Asp Ile Arg Tyr Leu Gly Lys Ile Phe Ser Ser Ala Thr Ser Leu Arg																		
835 840 845																		
ctg caa ata aag aga tgt gct ggt gtg gct gga agc ctc agt ttg gtc	2592																	
Leu Gln Ile Lys Arg Cys Ala Gly Val Ala Gly Ser Leu Ser Leu Val																		
850 855 860																		
ctc agc acc tgt aag aac att tat tct ctc atg gtg gaa gcc agt ccc	2640																	
Leu Ser Thr Cys Lys Asn Ile Tyr Ser Leu Met Val Glu Ala Ser Pro																		
865 870 875 880																		
ctc acc ata gaa gat gag agg cac atc aca tct gta aca aac ctg aaa	2688																	
Leu Thr Ile Glu Asp Glu Arg His Ile Thr Ser Val Thr Asn Leu Lys																		
885 890 895																		
acc ttg agt att cat gac cta cag aat caa cgg ctg ccg ggt ggt ctg	2736																	
Thr Leu Ser Ile His Asp Leu Gln Asn Gln Arg Leu Pro Gly Gly Leu																		
900 905 910																		
act gac agc ttg ggt aac ttg aag aac ctt aca aag ctc ata atg gat	2784																	
Thr Asp Ser Leu Gly Asn Leu Lys Asn Leu Thr Lys Leu Ile Met Asp																		
915 920 925																		
aac ata aag atg aat gaa gaa gat gct ata aaa cta gct gaa ggc ctg	2832																	
Asn Ile Lys Met Asn Glu Glu Asp Ala Ile Lys Leu Ala Glu Gly Leu																		
930 935 940																		
aaa aac ctg aag aag atg tgt tta ttt cat ttg acc cac ttg tct gac	2880																	
Lys Asn Leu Lys Lys Met Cys Leu Phe His Leu Thr His Leu Ser Asp																		
945 950 955 960																		
att gga gag gga atg gat tac ata gtc aag tct ctg tca agt gaa ccc	2928																	
Ile Gly Glu Gly Met Asp Tyr Ile Val Lys Ser Leu Ser Ser Glu Pro																		
965 970 975																		

tgt gac ctt gaa gaa att caa tta gtc tcc tgc tgc ttg tct gca aat	2976
Cys Asp Leu Glu Glu Ile Gln Leu Val Ser Cys Cys Leu Ser Ala Asn	
980 985 990	
gca gtg aaa atc cta gct cag aat ctt cac aat ttg gtc aaa ctg agc	3024
Ala Val Lys Ile Leu Ala Gln Asn Leu His Asn Leu Val Lys Leu Ser	
995 1000 1005	
att ctt gat tta tca gaa aat tac ctg gaa aaa gat gga aat gaa gct	3072
Ile Leu Asp Leu Ser Glu Asn Tyr Leu Glu Lys Asp Gly Asn Glu Ala	
1010 1015 1020	
ctt cat gaa ctg atc gac agg atg aac gtg cta gaa cag ctc acc gca	3120
Leu His Glu Leu Ile Asp Arg Met Asn Val Leu Glu Gln Leu Thr Ala	
1025 1030 1035 1040	
ctg atg ctg ccc tgg ggc tgt gac gtg caa ggc agc ctg agc agc ctg	3168
Leu Met Leu Pro Trp Gly Cys Asp Val Gln Gly Ser Leu Ser Ser Leu	
1045 1050 1055	
ttg aaa cat ttg gag gag gtc cca caa ctc gtc aag ctt ggg ttg aaa	3216
Leu Lys His Leu Glu Glu Val Pro Gln Leu Val Lys Leu Gly Leu Lys	
1060 1065 1070	
aac tgg aga ctc aca gat aca gag att aga att tta ggt gca ttt ttt	3264
Asn Trp Arg Leu Thr Asp Thr Glu Ile Arg Ile Leu Gly Ala Phe Phe	
1075 1080 1085	
gga aag aac cct ctg aaa aac ttc cag cag ttg aat ttg gcg gga aat	3312
Gly Lys Asn Pro Leu Lys Asn Phe Gln Gln Leu Asn Leu Ala Gly Asn	
1090 1095 1100	
cgt gtg agc agt gat gga tgg ctt gcc ttc atg ggt gta ttt gag aat	3360
Arg Val Ser Ser Asp Gly Trp Leu Ala Phe Met Gly Val Phe Glu Asn	
1105 1110 1115 1120	
ctt aag caa tta gtg ttt ttt gac ttt agt act aaa gaa ttt cta cct	3408
Leu Lys Gln Leu Val Phe Phe Asp Phe Ser Thr Lys Glu Phe Leu Pro	
1125 1130 1135	
gat cca gca tta gtc aga aaa ctt agc caa gtg tta tcc aag tta act	3456
Asp Pro Ala Leu Val Arg Lys Leu Ser Gln Val Leu Ser Lys Leu Thr	
1140 1145 1150	
ttt ctg caa gaa gct agg ctt gtt ggg tgg caa ttt gat gat gat gat	3504
Phe Leu Gln Glu Ala Arg Leu Val Gly Trp Gln Phe Asp Asp Asp Asp	
1155 1160 1165	
ctc agt gtt att aca gat gag aaa gct cag atg att tgc cca tgg gtt	3552
Leu Ser Val Ile Thr Asp Glu Lys Ala Gln Met Ile Cys Pro Trp Val	
1170 1175 1180	
ata aaa cta ctt cct tac aca gtg gca gca tca gaa ctg gaa ttc aga	3600
Ile Lys Leu Leu Pro Tyr Thr Val Ala Ala Ser Glu Leu Glu Phe Arg	
1185 1190 1195 1200	

tct ctt gcc tcc tag  
Ser Leu Ala Ser

3615

<210> 5  
<211> 1204  
<212> PRT  
<213> Homo sapiens

<400> 5  
Met Leu Asn Ala Gly Pro Leu Gly Ser Leu Ile Ser Phe Ser Ile Leu  
1 5 10 15  
Cys Leu Cys Val Phe Phe Phe Ser Lys Ser Leu Val Pro Pro Asn Glu  
20 25 30  
Lys His Pro Gln Asn Lys Lys Val Ser Gly Leu Gln Glu Leu Glu Ala  
35 40 45  
Ser Leu Lys Arg Lys Ala Asn Thr Lys Lys Leu Tyr Phe Lys Asn Met  
50 55 60  
Ser Trp Ser Pro Lys Lys Arg Ala Ile Gly Leu Leu Ser Gln Arg Pro  
65 70 75 80  
Leu Gln Ala Asp Thr Gln Ala Ala Gly Arg Arg Glu Glu His Ile Gly  
85 90 95  
Gly Arg Thr Tyr Lys Gln Leu Asp Val Gln Arg Thr Leu Lys Gly Glu  
100 105 110  
Cys Trp Arg Lys Ser Thr Gln Gln Thr Ser Ala Arg Gln Gln Ala Ile  
115 120 125  
His Gln Arg Asn Asp Ser Glu Phe Gly Leu Glu Val Asn Phe Ile Lys  
130 135 140  
Asp Asn Ser Arg Ala Leu Ile Gln Arg Met Gly Met Thr Val Ile Lys  
145 150 155 160  
Gln Ile Thr Asp Asp Leu Phe Val Trp Asn Val Leu Asn Arg Glu Glu  
165 170 175  
Val Asn Ile Ile Cys Cys Glu Lys Val Glu Gln Asp Ala Ala Arg Gly  
180 185 190  
Ile Ile His Met Ile Leu Lys Lys Gly Ser Glu Ser Cys Asn Leu Phe  
195 200 205  
Leu Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu Phe Gln Asp Leu Asn  
210 215 220  
Gly Gln Ser Phe Glu Glu Thr Gln Asn Trp Val Phe Phe Asn Ile Thr  
225 230 235 240  
Ser Ser Leu Ile Gly Leu Phe His Gln Thr Ser Glu Gly Asp Leu Asp  
245 250 255  
Asp Leu Ala Gln Asp Leu Lys Asp Leu Tyr His Thr Pro Ser Phe Leu  
260 265 270  
Asn Phe Tyr Pro Leu Gly Glu Asp Ile Asp Ile Ile Phe Asn Leu Lys  
275 280 285  
Ser Thr Phe Thr Glu Pro Val Leu Trp Arg Lys Asp Gln His His His  
290 295 300  
Arg Val Glu Gln Leu Thr Leu Asn Gly Leu Leu Gln Ala Leu Gln Ser  
305 310 315 320  
Pro Cys Ile Ile Glu Gly Glu Ser Gly Lys Gly Lys Ser Thr Leu Leu  
325 330 335  
Gln Arg Ile Ala Met Leu Trp Gly Ser Gly Lys Cys Lys Ala Leu Thr  
340 345 350  
Lys Phe Lys Phe Val Phe Phe Leu Arg Leu Ser Arg Ala Gln Gly Gly  
355 360 365

Leu	Phe	Glu	Thr	Leu	Cys	Asp	Gln	Leu	Leu	Asp	Ile	Pro	Gly	Thr	Ile	370	375	380
Arg	Lys	Gln	Thr	Phe	Met	Ala	Met	Leu	Leu	Lys	Leu	Arg	Gln	Arg	Val	385	390	395
Leu	Phe	Leu	Leu	Asp	Gly	Tyr	Asn	Glu	Phe	Lys	Pro	Gln	Asn	Cys	Pro	405	410	415
Glu	Ile	Glu	Ala	Leu	Ile	Lys	Glu	Asn	His	Arg	Phe	Lys	Asn	Met	Val	420	425	430
Ile	Val	Thr	Thr	Thr	Thr	Glu	Cys	Leu	Arg	His	Ile	Arg	Gln	Phe	Gly	435	440	445
Ala	Leu	Thr	Ala	Glu	Val	Gly	Asp	Met	Thr	Glu	Asp	Ser	Ala	Gln	Ala	450	455	460
Leu	Ile	Arg	Glu	Val	Leu	Ile	Lys	Glu	Leu	Ala	Glu	Gly	Leu	Leu	Leu	465	470	475
Gln	Ile	Gln	Lys	Ser	Arg	Cys	Leu	Arg	Asn	Leu	Met	Lys	Thr	Pro	Leu	485	490	495
Phe	Val	Val	Ile	Thr	Cys	Ala	Ile	Gln	Met	Gly	Glu	Ser	Glu	Phe	His	500	505	510
Ser	His	Thr	Gln	Thr	Thr	Leu	Phe	His	Thr	Phe	Tyr	Asp	Leu	Leu	Ile	515	520	525
Gln	Lys	Asn	Lys	His	Lys	His	Lys	Gly	Val	Ala	Ala	Ser	Asp	Phe	Ile	530	535	540
Arg	Ser	Leu	Asp	His	Cys	Gly	Asp	Leu	Ala	Leu	Glu	Gly	Val	Phe	Ser	545	550	555
His	Lys	Phe	Asp	Phe	Glu	Leu	Gln	Asp	Val	Ser	Ser	Val	Asn	Glu	Asp	565	570	575
Val	Leu	Leu	Thr	Thr	Gly	Leu	Leu	Cys	Lys	Tyr	Thr	Ala	Gln	Arg	Phe	580	585	590
Lys	Pro	Lys	Tyr	Lys	Phe	Phe	His	Lys	Ser	Phe	Gln	Glu	Tyr	Thr	Ala	595	600	605
Gly	Arg	Arg	Leu	Ser	Ser	Leu	Leu	Thr	Ser	His	Glu	Pro	Glu	Glu	Val	610	615	620
Thr	Lys	Gly	Asn	Gly	Tyr	Leu	Gln	Lys	Met	Val	Ser	Ile	Ser	Asp	Ile	625	630	635
Thr	Ser	Thr	Tyr	Ser	Ser	Leu	Leu	Arg	Tyr	Thr	Cys	Gly	Ser	Ser	Val	645	650	655
Glu	Ala	Thr	Arg	Ala	Val	Met	Lys	His	Leu	Ala	Ala	Val	Tyr	Gln	His	660	665	670
Gly	Cys	Leu	Leu	Gly	Leu	Ser	Ile	Ala	Lys	Arg	Pro	Leu	Trp	Arg	Gln	675	680	685
Glu	Ser	Leu	Gln	Ser	Val	Lys	Asn	Thr	Thr	Glu	Gln	Glu	Ile	Leu	Lys	690	695	700
Ala	Ile	Asn	Ile	Asn	Ser	Phe	Val	Glu	Cys	Gly	Ile	His	Leu	Tyr	Gln	705	710	715
Glu	Ser	Thr	Ser	Lys	Ser	Ala	Leu	Ser	Gln	Glu	Phe	Glu	Ala	Phe	Phe	725	730	735
Gln	Gly	Lys	Ser	Leu	Tyr	Ile	Asn	Ser	Gly	Asn	Ile	Pro	Asp	Tyr	Leu	740	745	750
Phe	Asp	Phe	Phe	Glu	His	Leu	Pro	Asn	Cys	Ala	Ser	Ala	Leu	Asp	Phe	755	760	765
Ile	Lys	Leu	Asp	Phe	Tyr	Gly	Gly	Ala	Met	Ala	Ser	Trp	Glu	Lys	Ala	770	775	780
Ala	Glu	Asp	Thr	Gly	Gly	Ile	His	Met	Glu	Glu	Ala	Pro	Glu	Thr	Tyr	785	790	795
Ile	Pro	Ser	Arg	Ala	Val	Ser	Leu	Phe	Phe	Asn	Trp	Lys	Gln	Glu	Phe	805	810	815
Arg	Thr	Leu	Glu	Val	Thr	Leu	Arg	Asp	Phe	Ser	Lys	Leu	Asn	Lys	Gln			



				820				825				830			
Asp	Ile	Arg	Tyr	Leu	Gly	Lys	Ile	Phe	Ser	Ser	Ala	Thr	Ser	Leu	Arg
				835				840				845			
Leu	Gln	Ile	Lys	Arg	Cys	Ala	Gly	Val	Ala	Gly	Ser	Leu	Ser	Leu	Val
				850				855				860			
Leu	Ser	Thr	Cys	Lys	Asn	Ile	Tyr	Ser	Leu	Met	Val	Glu	Ala	Ser	Pro
				865				870				875			
Leu	Thr	Ile	Glu	Asp	Glu	Arg	His	Ile	Thr	Ser	Val	Thr	Asn	Leu	Lys
				885				890				895			
Thr	Leu	Ser	Ile	His	Asp	Leu	Gln	Asn	Gln	Arg	Leu	Pro	Gly	Gly	Leu
				900				905				910			
Thr	Asp	Ser	Leu	Gly	Asn	Leu	Lys	Asn	Leu	Thr	Lys	Leu	Ile	Met	Asp
				915				920				925			
Asn	Ile	Lys	Met	Asn	Glu	Glu	Asp	Ala	Ile	Lys	Leu	Ala	Glu	Gly	Leu
				930				935				940			
Lys	Asn	Leu	Lys	Lys	Met	Cys	Leu	Phe	His	Leu	Thr	His	Leu	Ser	Asp
				945				950				955			
Ile	Gly	Glu	Gly	Met	Asp	Tyr	Ile	Val	Lys	Ser	Leu	Ser	Ser	Glu	Pro
				965				970				975			
Cys	Asp	Leu	Glu	Glu	Ile	Gln	Leu	Val	Ser	Cys	Cys	Leu	Ser	Ala	Asn
				980				985				990			
Ala	Val	Lys	Ile	Leu	Ala	Gln	Asn	Leu	His	Asn	Leu	Val	Lys	Leu	Ser
				995				1000				1005			
Ile	Leu	Asp	Leu	Ser	Glu	Asn	Tyr	Leu	Glu	Lys	Asp	Gly	Asn	Glu	Ala
				1010				1015				1020			
Leu	His	Glu	Leu	Ile	Asp	Arg	Met	Asn	Val	Leu	Glu	Gln	Leu	Thr	Ala
				1025				1030				1035			
Leu	Met	Leu	Pro	Trp	Gly	Cys	Asp	Val	Gln	Gly	Ser	Leu	Ser	Ser	Leu
				1045				1050				1055			
Leu	Lys	His	Leu	Glu	Glu	Val	Pro	Gln	Leu	Val	Lys	Leu	Gly	Leu	Lys
				1060				1065				1070			
Asn	Trp	Arg	Leu	Thr	Asp	Thr	Glu	Ile	Arg	Ile	Leu	Gly	Ala	Phe	Phe
				1075				1080				1085			
Gly	Lys	Asn	Pro	Leu	Lys	Asn	Phe	Gln	Gln	Leu	Asn	Leu	Ala	Gly	Asn
				1090				1095				1100			
Arg	Val	Ser	Ser	Asp	Gly	Trp	Leu	Ala	Phe	Met	Gly	Val	Phe	Glu	Asn
				1105				1110				1115			
Leu	Lys	Gln	Leu	Val	Phe	Phe	Asp	Phe	Ser	Thr	Lys	Glu	Phe	Leu	Pro
				1125				1130				1135			
Asp	Pro	Ala	Leu	Val	Arg	Lys	Leu	Ser	Gln	Val	Leu	Ser	Lys	Leu	Thr
				1140				1145				1150			
Phe	Leu	Gln	Glu	Ala	Arg	Leu	Val	Gly	Trp	Gln	Phe	Asp	Asp	Asp	Asp
				1155				1160				1165			
Leu	Ser	Val	Ile	Thr	Asp	Glu	Lys	Ala	Gln	Met	Ile	Cys	Pro	Trp	Val
				1170				1175				1180			
Ile	Lys	Leu	Leu	Pro	Tyr	Thr	Val	Ala	Ala	Ser	Glu	Leu	Glu	Phe	Arg
				1185				1190				1195			
Ser	Leu	Ala	Ser												

&lt;210&gt; 6

&lt;211&gt; 3612

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 6

atgctgaacg ctggccccct gggctccctt atttttttct ctatactttg tctctgtgtc

60

tttttctttt	ccaagtctct	cgttccacct	aacgagaaac	acccacagaa	caagaaggta	120
tctggtctac	aagaactcga	ggcctcactg	aaacggaaa	caaatacaaa	gaaactttat	180
tttaaaaaca	tgtcttggtc	tcccaagaag	agggcaattg	gattgctcag	ccagagaccc	240
ttgcaggcag	acacacaagc	ggctggacgt	cgagaggaac	acatcggcgg	aagaacatac	300
aagcagctgg	acgtccagag	gacgttgaag	ggagaatgct	ggcggagag	cacacaacag	360
acatcggcac	gccagcaggc	catccaccag	aggaacgact	cggagtttgg	cctggagggtg	420
aatttcataa	aggacaatag	ccgagccctt	attcaaagaa	tgggaatgac	tgttataaag	480
caaatcacag	atgacctatt	tgtatggaat	gttctgaatc	gcgaagaagt	aaacatcatt	540
tgctgcgaga	aggtggagca	ggatgctgct	agagggatca	ttcacatgat	tttgaaaaag	600
ggttcagagt	cctgtaacct	ctttcttaaa	tcccttaagg	agtggaaacta	tcctctattt	660
caggacttga	atggacaaa	ttttgaggag	acacagaatt	gggtcttctt	taacatcacc	720
tcttctctaa	taggtctttt	tcatcagaca	tcagaaggag	acttggacga	tttggctcag	780
gatttaaagg	acttgtacca	taccccatct	tttctgaact	tttatccctt	tggatgaagat	840
attgacatta	tttttaactt	gaaaagcacc	ttcacagaac	ctgtcctgtg	gaggaaggac	900
caacaccatc	accgcgtgga	gcagctgacc	ctgaatggcc	tcctgcaggc	tccttcagagc	960
ccctgcatca	ttgaagggga	atctggcaaa	ggcaagtcca	ctctgctgca	gcgaattgcc	1020
atgctctggg	gctccggaaa	gtgcaaggct	ctgaccaagt	tcaaattcgt	cttcttcctc	1080
cgtctcagca	gggcccagg	tggacttttt	gaaacctctt	gtgatcaact	cctggatata	1140
cctggcaca	tcaggaagca	gacattcatg	gccatgctgc	tgaagctgcg	gcagaggggtt	1200
cttttcttct	ttgatggcta	caatgaattc	aagccccaga	actgcccaga	aatcgaagcc	1260
ctgataaagg	aaaaccaccg	cttcaagaac	atggtcatcg	tcaccactac	cactgagtgc	1320
ctgaggcaca	tacggcagtt	tgggtgccctg	actgctgagg	tgggggatat	gacagaagac	1380
agcggccagg	ctctcatccg	agaagtgtctg	atcaaggagc	ttgctgaagg	cttgttgctc	1440
caaattcaga	aatccagggtg	cttgaggaat	ctcatgaaga	cccctctctt	tgtggtcatc	1500
acttgtgcaa	tccagatggg	tgaaagtga	ttccactctc	acacacaaac	aacgctgttc	1560
cataccttct	atgatctgtt	gatacagaaa	aacaaacata	aacataaagg	tgtggctgca	1620
agtgaactca	tccggagcct	ggaccactgt	ggagaccctag	ctctggagg	tgtgttctcc	1680
cacaagtttg	atttcgaact	gcaggatgtg	tcagcgtga	atgaggatgt	cctgctgaca	1740
actgggctcc	tctgtaaata	tacagctcaa	aggttcaagc	caaagtataa	attctttcac	1800
aagtcatctc	aggagtacac	agcaggacga	agactcagca	gtttattgac	gtctcatgag	1860
ccagaggagg	tgaccaagg	gaatggttac	ttgcagaaaa	tggtttccat	ttcggacatt	1920
acatccactt	atagcagcct	gctccggtac	acctgtgggt	catctgtgga	agccaccagg	1980
gctgttatga	agcacctcgc	agcagtgtat	caacacggct	gccttctcgg	actttccatc	2040
gccaaagggc	ctctctggag	acaggaatct	ttgcaaagt	tgaaaaacac	cactgagcaa	2100
gaaattctga	aagccataaa	catcaattcc	tttgtagagt	gtggcatcca	tttatatcaa	2160
gagagtacat	ccaaatcagc	cctgagccaa	gaatttgaag	ctttctttca	aggtaaaagc	2220
ttatatatca	actcagggaa	catccccgat	tacttatattg	acttctttga	acatttgccc	2280
aattgtgcaa	gtgccctgga	cttcattaaa	ctggactttt	atgggggagc	tatggcttca	2340
tgggaaaagg	ctgcagaaga	cacagggtga	atccacatgg	aagaggcccc	agaaacctac	2400
attcccagca	gggctgtatc	tttgttcttc	aactggaagc	aggaattcag	gactctggag	2460
gtcacactcc	gggatttcag	caagttgaat	aagcaagata	tcagatatct	ggggaaaata	2520
ttcagctctg	ccacaagcct	caggctgcaa	ataaagagat	gtgctggtgt	ggctggaagc	2580
ctcagtttgg	tcctcagcac	ctgtaagaac	atttattctc	tcatggtgga	agccagtccc	2640
ctcaccatag	aagatgagag	gcacatcaca	tctgtaacaa	acctgaaaac	cttgagtatt	2700
catgacctac	agaatcaacg	gctgcggggt	ggtctgactg	acagcttggg	taacttgaag	2760
aaccttacaa	agctcataat	ggataacata	aagatgaatg	aagaagatgc	tataaaacta	2820
gctgaaggcc	tgaaaaacct	gaagaagatg	tgtttatttc	atttgaccca	cttgtctgac	2880
attggagagg	gaatggatta	catagtcaag	tctctgtcaa	gtgaaccttg	tgaccttgaa	2940
gaaattcaat	tagtctcctg	ctgcttgtct	gcaaatgcag	tgaaaatcct	agctcagaat	3000
cttcacaatt	tgggtcaaat	gagcattctt	gatttatcag	aaaattacct	ggaaaaagat	3060
ggaaatgaag	ctcttcatga	actgatcgac	aggatgaacg	tgctagaaca	gctcaccgca	3120
ctgatgctgc	cctggggctg	tgacgtgcaa	ggcagcctga	gcagcctgtt	gaaacatttg	3180
gaggagggtcc	cacaactcgt	caagcttggg	ttgaaaaact	ggagactcac	agatacagag	3240
attagaattt	taggtgcatt	ttttggaaag	aacctctga	aaaacttcca	gcagttgaat	3300
ttggcgggaa	atcgtgtgag	cagtgatgga	tggcttgccct	tcatgggtgt	atttgagaat	3360
cttaagcaat	tagtggtttt	tgacttttagt	actaaagaat	ttctacctga	tccagcatta	3420
gtcagaaaa	ttagccaagt	gttatccaag	ttaacttttc	tgcaagaagc	taggcttggt	3480

```

gggtggcaat ttgatgatga tgatctcagt gttattacag atgagaaagc tcagatgatt 3540
tgcccatggg ttataaaact acttccttac acagtggcag catcagaact ggaattcaga 3600
tctcttgccct cc 3612

```

```

<210> 7
<211> 90
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> consensus sequence

```

```

<400> 7
Ala Glu Asp Asp Arg Arg Leu Leu Arg Lys Asn Arg Leu Glu Leu Leu
 1             5             10             15
Gly Glu Leu Thr Leu Ser Gly Leu Leu Asp His Leu Leu Glu Lys Asn
      20             25             30
Val Leu Thr Glu Glu Glu Glu Glu Lys Ile Lys Ala Lys Asn Thr Thr
      35             40             45
Arg Arg Asp Lys Ala Arg Glu Leu Ile Asp Ser Val Gln Lys Lys Gly
      50             55             60
Asn Gln Ala Phe Gln Ile Phe Leu Gln Ala Leu Arg Glu Thr Asp Gln
65             70             75             80
Glu Leu Leu Ala Asp Leu Leu Leu Asp Glu
      85             90

```

```

<210> 8
<211> 23
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> consensus sequence

```

```

<400> 8
Asn Leu Glu Glu Leu Asp Leu Ser Asn Asn Leu Thr Ser Leu Pro Pro
 1             5             10             15
Gly Leu Phe Ser Asn Leu Pro
      20

```

```

<210> 9
<211> 781
<212> PRT
<213> Homo sapiens

```

```

<400> 9
Glu Leu Val Leu Pro Glu Val Phe Gly Asn Leu Asn Ser Val Met Cys
 1             5             10             15
Val Glu Gly Glu Ala Gly Ser Gly Lys Thr Val Leu Leu Lys Lys Ile
      20             25             30
Ala Phe Leu Trp Ala Ser Gly Cys Cys Pro Leu Leu Asn Arg Phe Gln
      35             40             45
Leu Val Phe Tyr Leu Ser Leu Ser Ser Thr Arg Pro Asp Glu Gly Leu
      50             55             60
Ala Ser Ile Ile Cys Asp Gln Leu Leu Glu Lys Glu Gly Ser Val Thr
65             70             75             80
Glu Met Cys Met Arg Asn Ile Ile Gln Gln Leu Lys Asn Gln Val Leu

```

			85					90				95			
Phe	Leu	Leu	Asp	Asp	Tyr	Lys	Glu	Ile	Cys	Ser	Ile	Pro	Gln	Val	Ile
			100					105					110		
Gly	Lys	Leu	Ile	Gln	Lys	Asn	His	Leu	Ser	Arg	Thr	Cys	Leu	Leu	Ile
		115					120					125			
Ala	Val	Arg	Thr	Asn	Arg	Ala	Arg	Asp	Ile	Arg	Arg	Tyr	Leu	Glu	Thr
	130					135					140				
Ile	Leu	Glu	Ile	Gln	Ala	Phe	Pro	Phe	Tyr	Asn	Thr	Val	Cys	Ile	Leu
145				150					155					160	
Arg	Lys	Leu	Phe	Ser	His	Asn	Met	Thr	Arg	Leu	Arg	Lys	Phe	Met	Val
			165					170					175		
Tyr	Phe	Gly	Lys	Asn	Gln	Ser	Leu	Gln	Lys	Ile	Gln	Lys	Thr	Pro	Leu
		180					185					190			
Phe	Val	Ala	Ala	Ile	Cys	Ala	His	Trp	Phe	Gln	Tyr	Pro	Phe	Asp	Pro
	195					200					205				
Ser	Phe	Asp	Asp	Val	Ala	Val	Phe	Lys	Ser	Tyr	Met	Glu	Arg	Leu	Ser
	210				215				220						
Leu	Arg	Asn	Lys	Ala	Thr	Ala	Glu	Ile	Leu	Lys	Ala	Thr	Val	Ser	Ser
225				230				235						240	
Cys	Gly	Glu	Leu	Ala	Leu	Lys	Gly	Phe	Phe	Ser	Cys	Cys	Phe	Glu	Phe
			245				250						255		
Asn	Asp	Asp	Asp	Leu	Ala	Glu	Ala	Gly	Val	Asp	Glu	Asp	Glu	Asp	Leu
		260				265					270				
Thr	Met	Cys	Leu	Met	Ser	Lys	Phe	Thr	Ala	Gln	Arg	Leu	Arg	Pro	Phe
	275					280					285				
Tyr	Arg	Phe	Leu	Ser	Pro	Ala	Phe	Gln	Glu	Phe	Leu	Ala	Gly	Met	Arg
	290				295				300						
Leu	Ile	Glu	Leu	Leu	Asp	Ser	Asp	Arg	Gln	Glu	His	Gln	Asp	Leu	Gly
305				310				315						320	
Leu	Tyr	His	Leu	Lys	Gln	Ile	Asn	Ser	Pro	Met	Met	Thr	Val	Ser	Ala
			325				330						335		
Tyr	Asn	Asn	Phe	Leu	Asn	Tyr	Val	Ser	Ser	Leu	Pro	Ser	Thr	Lys	Ala
	340					345					350				
Gly	Pro	Lys	Ile	Val	Ser	His	Leu	Leu	His	Leu	Val	Asp	Asn	Lys	Glu
	355					360					365				
Ser	Leu	Glu	Asn	Ile	Ser	Glu	Asn	Asp	Asp	Tyr	Leu	Lys	His	Gln	Pro
	370				375				380						
Glu	Ile	Ser	Leu	Gln	Met	Gln	Leu	Leu	Arg	Gly	Leu	Trp	Gln	Ile	Cys
385				390				395						400	
Pro	Gln	Ala	Tyr	Phe	Ser	Met	Val	Ser	Glu	His	Leu	Leu	Val	Leu	Ala
		405					410						415		
Leu	Lys	Thr	Ala	Tyr	Gln	Ser	Asn	Thr	Val	Ala	Ala	Cys	Ser	Pro	Phe
	420					425						430			
Val	Leu	Gln	Phe	Leu	Gln	Gly	Arg	Thr	Leu	Thr	Leu	Gly	Ala	Leu	Asn
	435					440					445				
Leu	Gln	Tyr	Phe	Phe	Asp	His	Pro	Glu	Ser	Leu	Ser	Leu	Leu	Arg	Ser
	450				455				460						
Ile	His	Phe	Ser	Ile	Arg	Gly	Asn	Lys	Thr	Ser	Pro	Arg	Ala	His	Phe
465				470				475						480	
Ser	Val	Leu	Glu	Thr	Cys	Phe	Asp	Lys	Ser	Gln	Val	Pro	Thr	Ile	Asp
		485				490					495				
Gln	Asp	Tyr	Ala	Ser	Ala	Phe	Glu	Pro	Met	Asn	Glu	Trp	Glu	Arg	Asn
	500					505					510				
Leu	Ala	Glu	Lys	Glu	Asp	Asn	Val	Lys	Ser	Tyr	Met	Asp	Met	Gln	Arg
	515				520						525				
Arg	Ala	Ser	Pro	Asp	Leu	Ser	Thr	Gly	Tyr	Trp	Lys	Leu	Ser	Pro	Lys
	530				535						540				

Gln Tyr Lys Ile Pro Cys Leu Glu Val Asp Val Asn Asp Ile Asp Val  
 545 550 555 560  
 Val Gly Gln Asp Met Leu Glu Ile Leu Met Thr Val Phe Ser Ala Ser  
 565 570 575  
 Gln Arg Ile Glu Leu His Leu Asn His Ser Arg Gly Phe Ile Glu Ser  
 580 585 590  
 Ile Arg Pro Ala Leu Glu Leu Ser Lys Ala Ser Val Thr Lys Cys Ser  
 595 600 605  
 Ile Ser Lys Leu Glu Leu Ser Ala Ala Glu Gln Glu Leu Leu Leu Thr  
 610 615 620  
 Leu Pro Ser Leu Glu Ser Leu Glu Val Ser Gly Thr Ile Gln Ser Gln  
 625 630 635 640  
 Asp Gln Ile Phe Pro Asn Leu Asp Lys Phe Leu Cys Leu Lys Glu Leu  
 645 650 655  
 Ser Val Asp Leu Glu Gly Asn Ile Asn Val Phe Ser Val Ile Pro Glu  
 660 665 670  
 Glu Phe Pro Asn Phe His His Met Glu Lys Leu Leu Ile Gln Ile Ser  
 675 680 685  
 Ala Glu Tyr Asp Pro Ser Lys Leu Val Ala Ser Leu Pro Asn Phe Ile  
 690 695 700  
 Ser Leu Lys Ile Leu Asn Leu Glu Gly Gln Gln Phe Pro Asp Glu Glu  
 705 710 715 720  
 Thr Ser Glu Lys Phe Ala Tyr Ile Leu Gly Ser Leu Ser Asn Leu Glu  
 725 730 735  
 Glu Leu Ile Leu Pro Thr Gly Asp Gly Ile Tyr Arg Val Ala Lys Leu  
 740 745 750  
 Ile Ile Gln Gln Cys Gln Gln Leu His Cys Leu Arg Val Leu Ser Phe  
 755 760 765  
 Phe Lys Thr Leu Asn Asp Asp Ser Val Val Glu Ile Gly  
 770 775 780

<210> 10

<211> 202

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<400> 10

Glu Leu Leu Leu Ser Glu Gly Glu Gly Gly Lys Leu Leu Ile Ala Leu  
 1 5 10 15  
 Trp Ser Gly Cys Leu Phe Val Phe Leu Ser Arg Gly Leu Cys Asp  
 20 25 30  
 Gln Leu Leu Gly Leu Val Leu Phe Leu Leu Asp Tyr Glu Cys Ile Leu  
 35 40 45  
 Ile Asn His Thr Arg Ile Arg Glu Arg Lys Leu Lys Thr Pro Leu Phe  
 50 55 60  
 Val Cys Ala Phe Phe Leu Asn Lys Ala Cys Gly Leu Ala Leu Gly Phe  
 65 70 75 80  
 Ser Phe Phe Asp Val Glu Asp Leu Thr Leu Lys Thr Ala Gln Arg Pro  
 85 90 95  
 Tyr Phe Phe Gln Glu Ala Gly Arg Leu Leu Leu Ser Glu Gly Leu Ser  
 100 105 110  
 Ser Tyr Leu Tyr Ser Ala His Leu Leu Ser Leu Gln Leu Gln Val Tyr  
 115 120 125  
 Gln Thr Phe Gln Gly Leu Asn Tyr Phe Phe His Pro Ser Leu Ile Gly

130		135		140
Pro Tyr Ala Trp Glu Leu Ile Cys Leu Val Ser Gln Arg Leu Ser Ile				
145		150		155
Lys Cys Leu Ser Ser Leu Ser Leu Glu Gln Asn Leu Lys Leu Leu Glu				160
		165		170
Gly Asn Ile Leu Ser Leu Leu Leu Leu Asp Glu Ala Leu Asn Leu				175
		180		185
Leu Gly Lys Leu Leu Leu Phe Asp Asp Ile				190
195		200		

<210> 11  
 <211> 898  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> majority sequence

<400> 11

Glu Gln Leu Val Leu Asn Gly Val Leu Gly Ala Leu Asn Ser Val Cys				
1	5	10	15	
Ile Val Glu Gly Glu Ala Gly Ser Gly Lys Ser Val Leu Leu Gln Lys				
	20	25	30	
Ile Ala Phe Leu Trp Gly Ser Gly Lys Cys Lys Ala Leu Thr Lys Phe				
	35	40	45	
Gln Leu Val Phe Phe Leu Ser Leu Ser Ser Thr Arg Ala Asp Gly Gly				
	50	55	60	
Leu Ala Ser Ile Leu Cys Asp Gln Leu Leu Asp Ile Glu Gly Ser Val				
65	70	75	80	
Thr Glu Gln Thr Phe Arg Ala Ile Leu Leu Gln Leu Lys Asn Gln Val				
	85	90	95	
Leu Phe Leu Leu Asp Gly Tyr Asn Glu Ile Lys Pro Gln Asn Cys Ser				
	100	105	110	
Ile Pro Gln Val Ile Gly Ala Leu Ile Gln Glu Asn His Leu Ser Lys				
	115	120	125	
Thr Cys Val Leu Val Ala Val Thr Thr Glu Arg Ala Arg Asp Ile Arg				
	130	135	140	
Gln Phe Gly Ala Leu Ile Ala Glu Val Gly Ala Phe Thr Glu Asp Ser				
145	150	155	160	
Ala Val Ala Leu Leu Arg Glu Val Leu Ile Lys Glu Leu Ala Glu Leu				
	165	170	175	
Arg Gly Leu Leu Val Gln Ile Gly Lys Ser Gln Ser Leu Gln Asn Leu				
	180	185	190	
Gln Lys Thr Pro Leu Phe Val Ala Ala Ile Cys Ala Ile Gln Trp Gly				
	195	200	205	
Glu Ser Glu Phe Asp Ser Ser Phe Thr Asp Val Ala Val Phe Lys Ser				
	210	215	220	
Phe Tyr Asp Leu Leu Ile Leu Lys Asn Lys His Lys His Gly Val Ala				
225	230	235	240	
Ala Ala Asp Ile Leu Lys Ala Thr Val Ser Ser Cys Gly Asp Leu Ala				
	245	250	255	
Leu Glu Gly Val Phe Ser His Lys Phe Asp Phe Glu Leu Asp Asp Val				
	260	265	270	
Ala Glu Ala Gly Val Asp Glu Asp Val Leu Leu Thr Thr Gly Leu Leu				
	275	280	285	
Ser Lys Phe Thr Ala Gln Arg Leu Lys Pro Lys Tyr Lys Phe Leu Ser				
290	295	300		

Lys	Ala	Phe	Gln	Glu	Phe	Leu	Ala	Gly	Arg	Arg	Leu	Ile	Ser	Leu	Leu
305					310					315					320
Thr	Ser	Asp	Glu	Gln	Glu	Glu	Val	Thr	Leu	Gly	Leu	Gly	His	Leu	Gln
			325						330					335	
Gln	Ile	Val	Ser	Ile	Ser	Asp	Ile	Val	Ser	Ala	Tyr	Ser	Ser	Leu	Leu
		340						345					350		
Asn	Tyr	Val	Ser	Gly	Leu	Ser	Ser	Val	Glu	Ala	Gly	Arg	Ala	Val	Val
	355						360					365			
Ser	His	Leu	Ala	Ala	Val	Val	Asp	Asn	Lys	Gly	Ser	Leu	Leu	Gly	Leu
	370					375					380				
Ser	Ile	Ala	Asp	Asp	Tyr	Leu	Lys	His	Gln	Glu	Ser	Ile	Ser	Leu	Gln
385					390					395					400
Met	Gln	Leu	Leu	Gln	Gly	Val	Lys	Asn	Ile	Thr	Glu	Gln	Ala	Ile	Leu
				405					410					415	
Ser	Ala	Val	Ser	Ile	Asn	Leu	Leu	Val	Leu	Ala	Gly	Ile	Thr	Ala	Tyr
		420						425					430		
Gln	Ser	Ser	Thr	Val	Ala	Ala	Ala	Leu	Ser	Gln	Val	Leu	Glu	Ala	Phe
		435					440					445			
Leu	Gln	Gly	Lys	Ser	Leu	Thr	Leu	Gly	Ala	Gly	Asn	Leu	Pro	Asp	Tyr
	450					455				460					
Leu	Phe	Asp	Phe	Phe	Asp	His	Leu	Pro	Glu	Ser	Ala	Ser	Ala	Leu	Asp
465					470					475					480
Ser	Ile	Lys	Leu	Ser	Ile	Arg	Gly	Gly	Ala	Thr	Ala	Ser	Arg	Ala	Lys
			485						490					495	
Ala	Ala	Val	Leu	Thr	Gly	Gly	Ile	Asp	Lys	Ser	Glu	Ala	Pro	Thr	Ile
		500						505					510		
Asp	Glu	Thr	Tyr	Ile	Pro	Ala	Ser	Ala	Val	Ser	Leu	Phe	Asn	Glu	Trp
		515					520					525			
Glu	Gln	Glu	Leu	Ala	Thr	Leu	Glu	Val	Thr	Val	Lys	Ser	Phe	Ser	Asp
	530					535					540				
Leu	Asn	Lys	Gln	Ala	Ile	Thr	Asp	Leu	Gly	Thr	Gly	Phe	Ser	Ser	Ala
545					550					555					560
Ser	Ser	Leu	Gln	Leu	Gln	Ile	Lys	Arg	Cys	Ala	Gly	Val	Ala	Gly	Ser
			565					570						575	
Leu	Ser	Leu	Val	Leu	Ser	Thr	Cys	Lys	Asn	Ile	Tyr	Ser	Leu	Glu	Val
		580						585					590		
Asp	Ala	Ser	Asp	Leu	Thr	Val	Val	Gly	Glu	Asp	His	Leu	Thr	Ile	Val
		595					600						605		
Thr	Asn	Leu	Thr	Val	Leu	Ser	Ile	His	Asp	Leu	Ala	Ser	Gln	Arg	Leu
	610					615					620				
Glu	Gly	Gly	Leu	Thr	Asp	Ser	Leu	Gly	Asn	Leu	Lys	Gly	Leu	Ile	Glu
625					630					635					640
Leu	Ile	Arg	Asp	Ala	Leu	Glu	Leu	Ser	Glu	Ala	Ser	Ala	Ile	Lys	Leu
			645						650					655	
Ala	Glu	Gly	Leu	Lys	Asn	Leu	Lys	Lys	Met	Cys	Leu	Ile	Ser	Leu	Leu
			660					665					670		
Glu	Leu	Ser	Ala	Ala	Gly	Glu	Gly	Leu	Leu	Leu	Ile	Val	Lys	Ser	Leu
		675					680					685			
Ser	Ser	Glu	Pro	Cys	Asp	Leu	Glu	Glu	Ile	Gln	Leu	Val	Ser	Cys	Cys
	690					695					700				
Leu	Val	Ala	Gly	Ala	Val	Gln	Ile	Leu	Ala	Gln	Ile	Leu	His	Asn	Leu
705					710					715					720
Val	Lys	Leu	Ser	Ile	Leu	Asp	Leu	Ser	Glu	Leu	Ser	Val	Asp	Leu	Asp
			725						730				735		
Gly	Asn	Ile	Ala	Val	His	Ser	Val	Ile	Pro	Asp	Glu	Phe	Asn	Val	Leu
		740						745					750		
Glu	Gln	Leu	Thr	Ala	Leu	Leu	Leu	Gln	Ile	Gly	Ala	Asp	Val	Asp	Gly

755		760		765
Ser Leu Ser Ser Leu Val	Ala Ser Leu Glu Glu Val	Ile Ser Leu Val		
770	775	780		
Ile Leu Gly Leu Glu Gly Gln Gln Leu Thr Asp Thr Glu Ile Ser Ile				
785	790	795	800	
Leu Gly Ala Phe Ile Gly Leu Gly Ser Leu Ser Asn Leu Glu Glu Leu				
805	810	815		
Ile Leu Ala Gly Gly Asp Val Ser Ser Asp Gly Trp Leu Ala Phe Met				
820	825	830		
Gly Val Phe Glu Val Ala Lys Leu Leu Val Phe Phe Asp Phe Ser Thr				
835	840	845		
Lys Glu Phe Leu Pro Asp Pro Ala Leu Val Gln Gln Leu Ser Gln Val				
850	855	860		
Leu Ser Val Leu Ser Phe Leu Gln Thr Ala Arg Leu Val Gly Trp Gln				
865	870	875	880	
Leu Asp Asp Asp Ser Val Val Val Ile Thr Gly Ala Phe Lys Leu Val				
885	890	895		

Thr Gly

<210> 12  
 <211> 3615  
 <212> DNA  
 <213> Homo sapiens

<400> 12

ctaggaggca	agagatctga	attccagttc	tgatgctgcc	actgtgtaag	gaagtagttt	60
tataacccat	gggcaaata	tctgagcttt	ctcatctgta	ataacactga	gatcatcatc	120
atcaaattgc	cacccaacaa	gcctagcttc	ttgcagaaaa	gttaacttgg	ataacacttg	180
gctaagtttt	ctgactaatg	ctggatcagg	tagaaattct	ttagtactaa	agtcaaaaaa	240
cactaattgc	ttaagattct	caaatacacc	catgaaggca	agccatccat	cactgctcac	300
acgatttccc	gccaaattca	actgctggaa	gtttttcaga	gggttctttc	caaaaaatgc	360
acctaaaatt	ctaattctctg	tatctgtgag	tctccagttt	ttcaacccaa	gcttgacgag	420
ttgtggggacc	tcttccaaat	gtttcaacag	gctgctcagg	ctgccttgca	cgtcacagcc	480
ccagggcagc	atcagtgcgg	tgagctgttc	tagcacgttc	atcctgtcga	tcagttcatg	540
aagagcttca	tttccatctt	tttccaggta	atcttctgat	aaatcaagaa	tgctcagttt	600
gaccaaattg	tgaagattct	gagctaggat	tttacttgca	tttgcagaca	agcagcagga	660
gactaattga	atttcttcaa	ggtcacaggg	ttcacttgac	agagacttga	ctatgtaatc	720
cattccctct	ccaatgtcag	acaagtgggt	caaatagaat	aaacacatct	tcttcagggt	780
tttcaggcct	tcagctagtt	ttatagcatc	ttcttcattc	atctttatgt	tatccattat	840
gagctttgta	aggttcttca	agttacccaa	gctgtcagtc	agaccaccgc	gcagccgttg	900
attctgtagg	tcatgaatac	tcaaggtttt	cagggtttgt	acagatgtga	tgtgcctctc	960
atcttctatg	gtgaggggac	tggttccac	catgagagaa	taaatgttct	tacaggtgct	1020
gaggaccaa	ctgaggcttc	cagccacacc	agcacatctc	tttatttgca	gctgaggct	1080
tgtggcagag	ctgaatat	tccccagata	tctgatattc	tgcttattca	acttgctgaa	1140
atcccggagt	gtgacctcca	gagtcctgaa	ttcctgcttc	cagttgaaga	acaaagatac	1200
agccctgctg	ggaatgtagg	tttctggggc	ctcttccatg	tggattccac	ctgtgtcttc	1260
tgcagccttt	tcccatgaag	ccatagctcc	cccataaaag	tccagtttaa	tgaagtccag	1320
ggcacttgca	caattgggca	aatgttcaaa	gaagtcaaat	aagtaatcgg	ggatgttccc	1380
tgagttgata	tataagcttt	taccttgaaa	gaaagcttca	aattcttggc	tcagggtctga	1440
tttggatgta	ctctcttgat	ataaatggat	gccacactct	acaaaggaat	tgatgtttat	1500
ggctttcaga	atttcttgct	cagtgggtgt	tttcacactt	tgcaaagatt	cctgtctcca	1560
gagaggcctc	ttggcgatgg	aaagtccgag	aaggcagccg	tgttgatata	ctgctgcgag	1620
gtgcttcata	acagccctgg	tggttccac	agatgacca	cagggtgtacc	ggagcaggct	1680
gctataagtg	gatgtaatgt	ccgaaatgga	aaccattttc	tgcaagtaac	cattccccct	1740
ggtcacctcc	tctgggtcat	gagacgtcaa	taaactgctg	agtcttcgtc	ctgctgtgta	1800
ctcctggaat	gacttgtgaa	agaatttata	ctttggcttg	aacctttgag	ctgtatatatt	1860



acagaggagc	ccagttgtca	gcaggacatc	ctcattcacg	ctggacacat	cctgcagttc	1920
gaaatcaaac	ttgtgggaga	acacaccctc	cagagctagg	tctccacagt	ggtccaggct	1980
ccgaatgaag	tcacttgag	ccacaccttt	atgtttgtgt	ttgtttttct	gtatcaacag	2040
atcatagaag	gtatggaaca	gcgttggttg	tgtgtgagag	tggaactcac	tttcacccat	2100
ctggattgca	caagtgatga	ccacaaagag	aggggtcttc	atgagattcc	tcaagcacct	2160
ggattttctga	atttgagca	acaagccttc	agcaagctcc	ttgatcagca	cttctcggat	2220
gagagcctgg	gcgctgtctt	ctgtcatatc	ccccacctca	gcagtcaggg	caccaaactg	2280
cgtatgtgc	ctcaggcact	cagtggtagt	ggtgacgatg	accatgttct	tgaagcggtg	2340
gttttctctt	atcagggtct	cgatttctgg	gcagttctgg	ggcttgaatt	cattgtagcc	2400
atcaagaagg	aaaagaacct	tctgccgcag	cttcagcagc	atggccatga	atgtctgctt	2460
cctgattgtg	ccaggatat	ccaggagtgt	atcacagagg	gtttcaaaaa	gtccaccctg	2520
ggccctgctg	agacggagga	agaagacgaa	tttgaacttg	gtcagagcct	tgcaactttcc	2580
ggagccccag	agcatggcaa	ttcgctgcag	cagagtggac	ttgcctttgc	cagattcccc	2640
ttcaatgatg	caggggtctt	gaagagcctg	caggaggcca	ttcagggta	gctgctccac	2700
gcggtgatgg	tggttgctct	tctccacag	gacaggttct	gtgaagggtg	ttttcaagtt	2760
aaaaataatg	tcaatatctt	caccaagggg	ataaaagtcc	agaaaagatg	gggtatggta	2820
caagtccctt	aaatcctgag	ccaaatcgtc	caagtctcct	tctgatgtct	gatgaaaaag	2880
acctattaga	gaagaggtga	tggttaaagaa	gacccaattc	tgtgtctcct	caaaactttg	2940
tccattcaag	tcctgaaata	gaggatagtt	ccactcctta	agggatttaa	gaaagagggt	3000
acaggactct	gaaccctttt	tcaaaatcat	gtgaatgatc	cctctagcag	catcctgctc	3060
caccttctcg	cagcaaatga	tgtttacttc	ttcgcgattc	agaacattcc	atacaaatag	3120
gtcatctgtg	atttgcttta	taacagtcac	tcccattctt	tgaataaggg	ctcggctatt	3180
gtcctttatg	aaattcacct	ccaggccaaa	ctccgagtcg	ttcctctggg	ggatggcctg	3240
ctggcgtgcc	gatgtctgtt	gtgtgctctt	ccgccagcat	tctcccttca	acgtcctctg	3300
gacgtccagc	tgcttgatg	ttcttcggcc	gatgtgttcc	tctcgacgtc	cagccgcttg	3360
tgtgtctgcc	tgcaagggtc	tctggctgag	caatccaatt	gccctcttct	tgggagacca	3420
agacatgttt	ttaaaataaa	gtttctttgt	atttgctttc	cgtttcagtg	aggcctcgag	3480
ttcttgtaga	ccagatacct	tcttgttctg	tgggtgtttc	tcgttaggtg	gaacgagaga	3540
cttggaagaa	aaaaagacac	agagacaaag	tatagagaaa	gaaataaggg	agcccagggg	3600
accagcgttc	agcat					3615